GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 7, 2006, 16:07:40 ; Search time 0.001 Seconds
                                              (without alignments)
                                              2331.684 Million cell updates/sec

Title: US-10-665-715-16-COPY
Perfect score: 2879
Sequence: 1 MEPDSVIEDKTIELMCSVPR.........PPSAQNETRSPSRTYTYISR 542

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 1 seqs, 2151 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-OUT=eliz.res -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6 -NO_XLPXY -NEG_SCORES=0
-LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10
-YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   y14153.gb_pr:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                  SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2384.5	82.8	2151	1	HSBTRCP	ACCESSION:Y14153
c 2	58	2.0	2151	1	HSBTRCP	ACCESSION:Y14153

                                 ALIGNMENTS

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RESULT 1
HSBTRCP
LOCUS           HSBTRCP                  2151 bp    mRNA    linear   PRI 07-FEB-2003
DEFINITION  Homo sapiens mRNA for beta-transducin repeat containing protein.
ACCESSION   Y14153
VERSION     Y14153.1  GI:2995193
KEYWORDS    beta-transducin repeats; beta-TRCP gene; WD repeat.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Margottin,F., Bour,S.P., Durand,H., Selig,L., Benichou,S.,
            Richard,V., Thomas,D., Strebel,K. and Benarous,R.
  TITLE     A novel human WD protein, h-beta TrCp, that interacts with HIV-1
            Vpu connects CD4 to the ER degradation pathway through an F-box
            motif
  JOURNAL   Mol. Cell 1 (4), 565-574 (1998)
  PUBMED    9660940
REFERENCE   2  (bases 1 to 2151)
  AUTHORS   Benarous,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JUL-1997) R. Benarous, INSERM - I.C.G.M., Laboratoire
            Interactions Proteiques, CHU Cochin, 24 rue de Fg.St-Jacques, 75014
            Paris, FRANCE
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /cell_line="Jurkat T-cell"
                     /cell_type="T lymphocyte"
                     /tissue_type="lymphoid"
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     CDS             70. .1779
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                     /codon_start=1
                     /product="beta-transducin repeats containing protein"
                     /protein_id="CAA74572.1"
                     /db_xref="GI:2995194"
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                     /db_xref="UniProtKB/Swiss-Prot:Q9Y297"
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                     LSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFK
                     NKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYD
                     DQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDV
                     NTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAA
                     VNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDN
                     TIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAG
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/rpt_unit_range=516. .544

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Best Local Similarity:  79.0%       Mismatches:    41
Query Match:            82.8%       Indels:        31
DB:                     1           Gaps:          7
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US-10-665-715-16-COPY (1-542) x HSBTRCP (1-2151)

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Qy        1 MetGluPro---AspSerValIleGluAspLysThrIleGluLeuMetCysSer------ 17
            |||:::|||    ::::::|||:::::::::::|||   ::::::  |||    |||
Db       70 ATGGACCCGGCCGAGGCGGTGCTGCAAGAGAAGGCACTCAAGTTTATGAATTCCTCAGAG 129


Qy       18 ------------------------------------ValPro--------------- 19
                                                :::|||
Db      130 AGAGAAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATACCAGAGAAGAATTCACTT 189


Qy       20 ArgSerLeuTrpLeuGlyCysAlaAsnLeuVal--------GluSerMetCysAlaLeu 36
            |||      :::   ||||||   |||        |||::::::|||
Db      190 AGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGTATGTTAGCA 249


Qy       37 SerCysLeuGlnSerMetProSerValArgCysLeu---------GlnIleSerAsnGly 53
            |||         :::|||    :::       |||:::        :::::::::::|||||
Db      250 AGC------ACTGCTATGAAGACTGAGAATTGTGTGGCCAAAACAAAACTTGCCAATGGC 303


Qy       54 ThrSerSerValIleValSerArgLysArgProSerGluGlyAsnTyrGlnLysGluLys 73
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Db      304 ACTTCCAGTATGATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTATGAAAAGGAAAAG 363


Qy       74 AspLeuCysIleLysTyrPheAspGlnTrpSerGluSerAspGlnValGluPheValGlu 93
            :::||||||:::||||||||||||:::||||||||||||||||||||||||||||||||||
Db      364 GAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTGGAATTTGTGGAA 423


Qy       94 HisLeuIleSerArgMetCysHisTyrGlnHisGlyHisIleAsnSerTyrLeuLysPro 113
            |||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||
Db      424 CATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCGTATCTTAAACCT 483


Qy      114 MetLeuGlnArgAspPheIleThrAlaLeuProGluGlnGlyLeuAspHisIleAlaGlu 133
            |||||||||||||||||||||||||||||||||||||||   :::||||||||||||||||
Db      484 ATGTTGCAGAGAGATTTCATAACTGCTCTGCCAGCTCGGGGATTGGATCATATCGCTGAG 543


Qy      134 AsnIleLeuSerTyrLeuAspAlaArgSerLeuCysAlaAlaGluLeuValCysLysGlu 153
            ||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||
Db      544 AACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGAACTTGTGTGCAAGGAA 603


Qy      154 TrpGlnArgValIleSerGluGlyMetLeuTrpLysLysLeuIleGluArgMetValArg 173
            |||      ||||||     |||:::||||||||||||||||||||||||||||||||||||
Db      604 TGGTACCGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAGAGAATGGTCAGG 663


Qy      174 ThrAspProLeuTrpLysGlyLeuSerGluArgArgGlyTrpAspGlnTyrLeuPheLys 193
            ||||||   ||||||:::||||||:::||||||||||||||||   ||||||||||||||
Db      664 ACAGATTCTCTGTGGAGAGGCCTGGCAGAACGAAGAGGATGGGGACAGTATTTATTCAAA 723
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Qy    194  AsnArgProThrAspGly------ProProAsnSerPheTyrArgSerLeuTyrProLys  211
           |||:::|||  ||||||     ||||||||||||||||||||||:::|||||||||||||
Db    724  AACAAACCTCCTGACGGGAATGCTCCTCCCAACTCTTTTTATAGAGCACTTTATCCTAAA  783

Qy    212  IleIleGlnAspIleGluThrIleGluSerAsnTrpArgCysGlyArgHisAsnLeuGln  231
           ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db    784  ATTATACAAGACATTGAGACAATAGAATCTAATTGGAGATGTGGAAGACATAGTTTACAG  843

Qy    232  ArgIleGlnCysArgSerGluAsnSerLysGlyValTyrCysLeuGlnTyrAspAspGlu  251
           ||||||   |||||||||||  |||||||||||||||||||||||||||||:::
Db    844  AGAATTCACTGCCGAAGTGAAACAAGCAAAGGAGTTTACTGTTTACAGTATGATGATCAG  903

Qy    252  LysIleIleSerGlyLeuArgAspAsnSerIleLysIleTrpAspLysThrSerLeuGlu  271
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Db    904  AAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATCTGGGATAAAAACACATTGGAA  963

Qy    272  CysLeuLysValLeuThrGlyHisThrGlySerValLeuCysLeuGlnTyrAspGluArg  291
           |||   :::::::|||||||||||||||||||||||||||||||||||||||||||||||||
Db    964  TGCAAGCGAATTCTCACAGGCCATACAGGTTCAGTCCTCTGTCTCCAGTATGATGAGAGA  1023

Qy    292  ValIleValThrGlySerSerAspSerThrValArgValTrpAspValAsnThrGlyGlu  311
           ||||||:::||||||||||||||||||||||||||||||||||||||||||||||||
Db    1024 GTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGATGTAAATACAGGTGAA  1083

Qy    312  ValLeuAsnThrLeuIleHisHisAsnGluAlaValLeuHisLeuArgPheSerAsnGly  331
           :::||||||||||||||||||||||||||   ||||||||||||||||||||:::||||||
Db    1084 ATGCTAAACACGTTGATTCACCATTGTGAAGCAGTTCTGCACTTGCGTTTCAATAATGGC  1143

Qy    332  LeuMetValThrCysSerLysAspArgSerIleAlaValTrpAspMetAlaSerAlaThr  351
           :::|||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db    1144 ATGATGGTGACCTGCTCCAAAGATCGTTCCATTGCTGTATGGGATATGGCCTCCCCAACT  1203

Qy    352  AspIleThrLeuArgArgValLeuValGlyHisArgAlaAlaValAsnValValAspPhe  371
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1204 GACATTACCCTCCGGAGGGTGCTGGTCGGACACCGAGCTGCTGTCAATGTTGTAGACTTT  1263

Qy    372  AspAspLysTyrIleValSerAlaSerGlyAspArgThrIleLysValTrpSerThrSer  391
           ||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db    1264 GATGACAAGTACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTATGGAACACAAGT  1323

Qy    392  ThrCysGluPheValArgThrLeuAsnGlyHisLysArgGlyIleAlaCysLeuGlnTyr  411
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1324 ACTTGTGAATTTGTAAGGACCTTAAATGGACACAAACGAGGCATTGCCTGTTTGCAGTAC  1383

Qy    412  ArgAspArgLeuValValSerGlySerSerAspAsnThrIleArgLeuTrpAspIleGlu  431
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1384 AGGGACAGGCTGGTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGACATAGAA  1443

Qy    432  CysGlyAlaCysLeuArgValLeuGluGlyHisGluGluLeuValArgCysIleArgPhe  451
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Db    1444 TGTGGTGCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTCGATTT  1503

Qy    452  AspAsnLysArgIleValSerGlyAlaTyrAspGlyLysIleLysValTrpAspLeuGln  471
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1504 GATAACAAGAGGATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTGTGGGATCTTGTG  1563

Qy    472  AlaAlaLeuAspProArgAlaProAlaSerThrLeuCysLeuArgThrLeuValGluHis  491
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Qy       492 SerGlyArgValPheArgLeuGlnPheAspGluPheGlnIleIleSerSerSerHisAsp 511
         |||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db      1624 TCCGGAAGAGTTTTTCGACTACAGTTTGATGAATTCCAGATTGTCAGTAGTTCACATGAT 1683

Qy       512 AspThrIleLeuIleTrpAspPheLeuAsnValProProSerAlaGlnAsnGluThrArg 531
         ||||||||||||||||||||||||||||   |||   :::                |||
Db      1684 GACACAATCCTCATCTGGGACTTCCTAAATGATCCAGCTGCCCAAGCTGAACCCCCCCGT 1743

Qy       532 SerProSerArgThrTyrThrTyrIleSerArg 542
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Db      1744 TCCCCTTCTCGAACATACACCTACATCTCCAGA 1776


RESULT 2
HSBTRCP/c
LOCUS          HSBTRCP                  2151 bp    mRNA    linear    PRI 07-FEB-2003
DEFINITION     Homo sapiens mRNA for beta-transducin repeat containing protein.
ACCESSION      Y14153
VERSION        Y14153.1  GI:2995193
KEYWORDS       beta-transducin repeats; beta-TRCP gene; WD repeat.
SOURCE         Homo sapiens (human)
  ORGANISM     Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE      1
  AUTHORS      Margottin,F., Bour,S.P., Durand,H., Selig,L., Benichou,S.,
               Richard,V., Thomas,D., Strebel,K. and Benarous,R.
  TITLE        A novel human WD protein, h-beta TrCp, that interacts with HIV-1
               Vpu connects CD4 to the ER degradation pathway through an F-box
               motif
  JOURNAL      Mol. Cell 1 (4), 565-574 (1998)
   PUBMED      9660940
REFERENCE      2  (bases 1 to 2151)
  AUTHORS      Benarous,R.
  TITLE        Direct Submission
  JOURNAL      Submitted (03-JUL-1997) R. Benarous, INSERM - I.C.G.M., Laboratoire
               Interactions Proteiques, CHU Cochin, 24 rue de Fg.St-Jacques, 75014
               Paris, FRANCE
FEATURES                Location/Qualifiers
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Alignment Scores:
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Best Local Similarity: 19.4%   Mismatches: 137
Query Match: 2.0%   Indels: 158
DB: 1   Gaps: 21

US-10-665-715-16-COPY (1-542) x HSBTRCP (1-2151)

Qy   20 ArgSerLeuTrpLeuGlyCysAlaAsnLeuValGluSerMetCysAlaLeuSerCysLeu 39
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Db   1970 AGACCGTCCTGGGCCGACTGCAGACCAACTGTGTCCCAACAGGAGTCTCAAAGC------ 1917

Qy   40 GlnSerMetProSerValArgCysLeuGlnIleSerAsnGlyThrSerSerValIleVal 59
                |||::: ||| :::||| |||:::||| :::::::
Db   1916 ---------CCTGCTCCTCGGCTAGTCCAGGG-AAACTGGGCAGTAGTTTGATTGTTACT 1867

Qy   60 SerArgLysArgProSerGluGlyAsnTyrGlnLysGluLysAspLeu------------ 75
                ||| ||| ||| ||| ::: |||
Db   1866 GTTGTTGCTCATCCTGGTATTGGCAGATACGTTAAATACCGCAA-CTTTAATGGGTCCTG 1808

Qy   76 ------------------------------------CysIleLysTyrPheAspGln 82
                                                 ||| |||:::::::
Db   1807 GGCAAGTATGAGGTCAGTGTATGGTTATTTATCTGGAGATGTAGGTGTATGTTCGAGAAG 1748

Qy   83 TrpSerGluSerAspGlnValGluPheValGluHisLeuIleSer---------ArgMet 99
             ::: |||:::   :::::::|||||| ||| :::
Db   1747 GGGAACGGGGGGGTTCAGCTTGGGCAGCTGGATCATTTAGGAAGTCCCAGATGAGGATTG 1688

Qy   100 CysHisTyrGlnHisGlyHisIleAsnSerTyrLeuLysProMetLeuGlnArgAspPhe 119
             |||||| |||:::||| ||| :::   :::   :::
Db   1687 TGTCAT-----------CATGTGAAC---TACTGACAATCTGGAATTCATCAAACTGTA 1643

Qy   120 IleThrAlaLeu------------ProGluGlnGlyLeuAspHisIleAlaGluAsnIle 135
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Db   1642 GTCGAAAAACTCTTCCGGAATGCTCCACAAGGGTCCGTAGACAGAGTGTCC-------- 1592

Qy   136 LeuSerTyrLeuAspAlaArgSerLeuCysAlaAlaGluLeuValCysLysGluTrpGln 155

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Db   1592 ----------------------------------------------------------- 1592

Qy    156 ArgValIleSerGluGlyMetLeuTrpLysLysLeuIleGluArgMetValArgThrAsp 175

Db   1592 ----------------------------------------------------------- 1592

Qy    176 ProLeuTrpLysGlyLeuSerGluArgArgGlyTrpAspGlnTyr-------------- 190
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Db   1591 --------------CTGCAGGAGCACGGGGGTCCAAAGCAGCCACAAGATCCCACACTT 1547

Qy    191 ---LeuPheLysAsnArg-ProThrAspGlyProProAsnSerPheTyrArgSerLeuTy 209
             |||    :::|||  |||||||||||                               ||
Db   1546 TAATTTTTCCATCATAGGCCCCACTGAC-----------------------------TA 1517

Qy    209 rProLysIleIleGlnAsp-IleGluThrIleGluSerAsnTrpArgCysGly------- 226
          ||||     :::|||:::    |||:::          |||:::|||
Db   1516 TCCTCTTGTTATCAAATCGAATACAACGCACCAATTCCTCATGGCCTTCTAACACTCGTA 1457

Qy    227 -------------------ArgHisAsnLeuGlnArgIleGlnCysArgSerGluAsnS 240
                             |||||||||
Db   1456 AACATGCACCACATTCTATGTCCCATAATCTG--------------------------- 1425

Qy    240 erLysGlyValTyrCysLeuGlnTyrAspAspGluLysIleIleSerGlyLeuArgAspA 260
                    :::       ||||||    :::    :::
Db   1424 ----------------ATAGTGTTGTCAGATGAGCCACTCACTACC------------- 1395

Qy    260 snSerIleLysIleTrpAspLysThrSerLeuGluCysLeu---------LysValLeuT 277
            |||:::     :::::::   |||   :::::::      |||       |||||||||
Db   1394 --AGCCTGTCCCTGTACTGCAAACAGGCAATGCCTCGTTTGTGTCCATTTAAGGTCCTTA 1337

Qy    277 hrGly-----------------HisThrGlySerValLeuCysLeuGlnTyrAspGluA 291
          ||                     ||||||         :::   |||      |||
Db   1336 CAAATTCACAAGTACTTGTGTTCCATACC------TTTATAGTTCTATCCCCAGATGCAG 1283

Qy    291 rgValIleValThrGlySerSerAspSerThrValArgValTrpAspValAsnThrGlyG 311
            :::       |||     :::|||:::                          |||
Db   1282 AAACAATGTACTTGTCATCAAAGTCTACAACATTGACAGCAGCTCGGTGTCCGACC---A 1226

Qy    311 luValLeuAsnThrLeuIleHisHisAsnGluAlaValLeuHisLeuArgPheSerAsnG 331
            |||       :::::::        ||||||:::    |||
Db   1225 GCACCCTCCGGAGGGTAATGTCAGTTGGGGAGGCCATATCCCATACAGCAATGGAACGAT 1166

Qy    331 lyLeu---MetValThrCys--------------SerLysAspArgSerIleAlaValT 345
          |||       ||||||                  |||   |||:::    :::    |
Db   1165 CTTTGGAGCAGGTCACCATCATGCCATTATTGAAACGCAAGTGCAGAACTGCTTCACAAT 1106

Qy    345 rpAspMetAlaSerAlaThrAspIleThrLeuArgArgValLeuValGlyHisArgAlaA 365
          ||     :::                  :::::::    |||          |||
Db   1105 GGTGAATC---------AACGTGTTTAGCATTTCACCTGTATTTACATCCCACACTCTG- 1056

Qy    365 laValAsnValValAspPheAspAspLysTyrIleValSerAlaSerGly---------A 382
             |||:::    ||||||         :::::::::::    |||
Db   1055 -------ACCGTGGAATCCGATGATCCTGTTATGATCACTCTCTCATCATACTGGAGAC 1004

Qy    382 spArgThrIleLysValTrp 388
            ||||||      ||||||
Db   1003 AGAGGACTGAACCTGTATGG 984
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Search completed: September 7, 2006, 16:07:41
Job time : 1 secs